

# SEQUENCE LISTING

<110> Burnham, Martin K. R.

<120> dexB

<130> GM10087

<150> 60/057,876

<151> 1997-09-02

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<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1608

<212> DNA

<213> Streptococcus pneumoniae

<220>

<221> CDS

<222> (1)...(1605)

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1				5					10					15	

aag agt ttt atg gat agt aat gga gat gga gtt ggt gat ttg cca ggt  
96

Lys	Ser	Phe	Met	Asp	Ser	Asn	Gly	Asp	Gly	Val	Gly	Asp	Leu	Pro	Gly
			20					25					30		

att acc agt aag ttg gac tat cta gct aag tta gga atc aca tcg att  
144

Ile Thr Ser Lys Leu Asp Tyr Leu Ala Lys Leu Gly Ile Thr Ser Ile

35

40

45

tgg ctt tct ccc gtt tat gac agc cct atg gat gat aat ggc tac gat  
192

Trp Leu Ser Pro Val Tyr Asp Ser Pro Met Asp Asp Asn Gly Tyr Asp  
50 55 60

att gct gat tat caa gcg att gcg gct att ttt gga acc atg gag gac  
240

Ile Ala Asp Tyr Gln Ala Ile Ala Ala Ile Phe Gly Thr Met Glu Asp  
65 70 75 80

atg gat gaa ctg att gca gaa gct aag aag cgt gat atc cgt atc atc  
288

Met Asp Glu Leu Ile Ala Glu Ala Lys Lys Arg Asp Ile Arg Ile Ile  
85 90 95

atg gac ttg gtg gtc aat cat acc tcg gat gag cat gcc tgg ttt gta  
336

Met Asp Leu Val Val Asn His Thr Ser Asp Glu His Ala Trp Phe Val  
100 105 110

gag gcc tgt gaa aat cct aat agc cct gag cga gac tac tat atc tgg  
384

Glu Ala Cys Glu Asn Pro Asn Ser Pro Glu Arg Asp Tyr Tyr Ile Trp  
115 120 125

cgc gat gaa ccc aat gac cta gat tct atc ttt agt ggg tct gct tgg  
432

Arg Asp Glu Pro Asn Asp Leu Asp Ser Ile Phe Ser Gly Ser Ala Trp  
130 135 140

gaa tac gat gaa aag tca ggt caa tac tat ctc cac ttt ttc agc aag  
480

Glu Tyr Asp Glu Lys Ser Gly Gln Tyr Tyr Leu His Phe Phe Ser Lys  
145 150 155 160

aaa cag ccg gat ctc aac tgg gaa aat gaa aaa ctt cgc cag aaa att  
528

Lys Gln Pro Asp Leu Asn Trp Glu Asn Glu Lys Leu Arg Gln Lys Ile

165

170

175

tat gag atg atg aac ttc tgg att gat aag ggt att ggt ggt ttc cgt  
576

Tyr Glu Met Met Asn Phe Trp Ile Asp Lys Gly Ile Gly Gly Phe Arg  
180 185 190

atg gat gtt att gac atg att ggc aaa att cct gac gag aag gta gtc  
624

Met Asp Val Ile Asp Met Ile Gly Lys Ile Pro Asp Glu Lys Val Val  
195 200 205

aat aat ggt cct atg ctc cat ccc tat ctc aag gaa atg aat cag gcg  
672

Asn Asn Gly Pro Met Leu His Pro Tyr Leu Lys Glu Met Asn Gln Ala  
210 215 220

acc ttt gga gat aag gat ctc ttg aca gta ggg gag act tgg gga gca  
720

Thr Phe Gly Asp Lys Asp Leu Leu Thr Val Gly Glu Thr Trp Gly Ala  
225 230 235 240

acg cca gag att gcc aaa ctc tac tct gat cca aag ggg caa gaa ttg  
768

Thr Pro Glu Ile Ala Lys Leu Tyr Ser Asp Pro Lys Gly Gln Glu Leu  
245 250 255

tct atg gtc ttc cag ttt gaa cat atc ggt ctt cag tat cag gaa ggt  
816

Ser Met Val Phe Gln Phe Glu His Ile Gly Leu Gln Tyr Gln Glu Gly  
260 265 270

cag cct aaa tgg cac tat caa aaa gag ctg aat atc gct aag tta aaa  
864

Gln Pro Lys Trp His Tyr Gln Lys Glu Leu Asn Ile Ala Lys Leu Lys  
275 280 285

gaa atc ttc aac aaa tgg cag aca gag tta gga gtt gag gac ggc tgg  
912

Glu Ile Phe Asn Lys Trp Gln Thr Glu Leu Gly Val Glu Asp Gly Trp

300

Asn Ser Leu Phe Trp Asn Asn His Asp Leu Pro Arg Ile Val Ser Ile  
305 310 315 320

Trp Gly Asn Asp Gln Glu Tyr Arg Glu Lys Ser Ala Lys Ala Phe Ala  
325 330 335

Ile Leu Leu His Leu Met Arg Gly Thr Pro Tyr Ile Tyr Gln Gly Glu  
340 345 350

Glu Ile Gly Met Thr Asn Tyr Pro Phe Glu Thr Leu Asp Gln Val Glu  
355 360 365

Asp Ile Glu Ser Leu Asn Tyr Ala Arg Glu Ala Leu Glu Lys Gly Val  
370 375 380

Pro Met Gln Glu Ile Met Asp Ser Ile Arg Val Ile Gly Arg Asp Asn  
385                    390                    395                    400

Ala Arg Thr Pro Met Gln Trp Asp Glu Ser Lys Asn Ala Gly Phe Ser  
405 410 415

Thr Gly Gln Pro Trp Leu Ala Val Asn Pro Asn Tyr Glu Met Ile Asn

[illegible]

420

425

430

gtc caa gaa gcg ctg gca aat cca gat tct att ttc tat acc tat cag  
1344

Val Gln Glu Ala Leu Ala Asn Pro Asp Ser Ile Phe Tyr Thr Tyr Gln  
435 440 445

aaa ctg gtc caa att cgc aag gag aat agt tgg cta att cga gct gac  
1392

Lys Leu Val Gln Ile Arg Lys Glu Asn Ser Trp Leu Ile Arg Ala Asp  
450 455 460

ttt gaa ttg ctt gat acg gct gat aag gtc ttt gct tat ata cgt aag  
1440

Phe Glu Leu Leu Asp Thr Ala Asp Lys Val Phe Ala Tyr Ile Arg Lys  
465 470 475 480

gat ggc gac cgt cgc ttc cta gtt gtg gct aac ttg tcc aat gaa gag  
1488

Asp Gly Asp Arg Arg Phe Leu Val Val Ala Asn Leu Ser Asn Glu Glu  
485 490 495

caa gac ttg aca gta gaa gga aaa gtc aaa tct gtc ttg att gaa aac  
1536

Gln Asp Leu Thr Val Glu Gly Lys Val Lys Ser Val Leu Ile Glu Asn  
500 505 510

acc cta gct caa gaa gtc ttt gaa aaa caa atc tta gtt cca tgg gat  
1584

Thr Leu Ala Gln Glu Val Phe Glu Lys Gln Ile Leu Val Pro Trp Asp  
515 520 525

gct ttc tgt gtg gaa tta cta taa  
1608

Ala Phe Cys Val Glu Leu Leu  
530 535

&lt;210&gt; 2

&lt;211&gt; 535

<212> PRT

<213> Streptococcus pneumoniae

<400> 2

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			20				25						30		
Ile	Thr	Ser	Lys	Leu	Asp	Tyr	Leu	Ala	Lys	Leu	Gly	Ile	Thr	Ser	Ile
		35					40					45			
Trp	Leu	Ser	Pro	Val	Tyr	Asp	Ser	Pro	Met	Asp	Asp	Asn	Gly	Tyr	Asp
	50					55					60				
Ile	Ala	Asp	Tyr	Gln	Ala	Ile	Ala	Ala	Ile	Phe	Gly	Thr	Met	Glu	Asp
65					70					75				80	
Met	Asp	Glu	Leu	Ile	Ala	Glu	Ala	Lys	Lys	Arg	Asp	Ile	Arg	Ile	Ile
				85					90					95	
Met	Asp	Leu	Val	Val	Asn	His	Thr	Ser	Asp	Glu	His	Ala	Trp	Phe	Val
			100						105					110	
Glu	Ala	Cys	Glu	Asn	Pro	Asn	Ser	Pro	Glu	Arg	Asp	Tyr	Tyr	Ile	Trp
		115					120					125			
Arg	Asp	Glu	Pro	Asn	Asp	Leu	Asp	Ser	Ile	Phe	Ser	Gly	Ser	Ala	Trp
	130					135						140			
Glu	Tyr	Asp	Glu	Lys	Ser	Gly	Gln	Tyr	Tyr	Leu	His	Phe	Phe	Ser	Lys
145					150					155					160
Lys	Gln	Pro	Asp	Leu	Asn	Trp	Glu	Asn	Glu	Lys	Leu	Arg	Gln	Lys	Ile
				165					170					175	
Tyr	Glu	Met	Met	Asn	Phe	Trp	Ile	Asp	Lys	Gly	Ile	Gly	Gly	Phe	Arg
			180					185						190	
Met	Asp	Val	Ile	Asp	Met	Ile	Gly	Lys	Ile	Pro	Asp	Glu	Lys	Val	Val
		195					200					205			
Asn	Asn	Gly	Pro	Met	Leu	His	Pro	Tyr	Leu	Lys	Glu	Met	Asn	Gln	Ala
	210					215						220			
Thr	Phe	Gly	Asp	Lys	Asp	Leu	Leu	Thr	Val	Gly	Glu	Thr	Trp	Gly	Ala
225					230					235					240
Thr	Pro	Glu	Ile	Ala	Lys	Leu	Tyr	Ser	Asp	Pro	Lys	Gly	Gln	Glu	Leu
				245					250					255	
Ser	Met	Val	Phe	Gln	Phe	Glu	His	Ile	Gly	Leu	Gln	Tyr	Gln	Glu	Gly
			260					265					270		
Gln	Pro	Lys	Trp	His	Tyr	Gln	Lys	Glu	Leu	Asn	Ile	Ala	Lys	Leu	Lys
		275					280						285		

Glu Ile Phe Asn Lys Trp Gln Thr Glu Leu Gly Val Glu Asp Gly Trp  
 290 295 300  
 Asn Ser Leu Phe Trp Asn Asn His Asp Leu Pro Arg Ile Val Ser Ile  
 305 310 315 320  
 Trp Gly Asn Asp Gln Glu Tyr Arg Glu Lys Ser Ala Lys Ala Phe Ala  
 325 330 335  
 Ile Leu Leu His Leu Met Arg Gly Thr Pro Tyr Ile Tyr Gln Gly Glu  
 340 345 350  
 Glu Ile Gly Met Thr Asn Tyr Pro Phe Glu Thr Leu Asp Gln Val Glu  
 355 360 365  
 Asp Ile Glu Ser Leu Asn Tyr Ala Arg Glu Ala Leu Glu Lys Gly Val  
 370 375 380  
 Pro Met Gln Glu Ile Met Asp Ser Ile Arg Val Ile Gly Arg Asp Asn  
 385 390 395 400  
 Ala Arg Thr Pro Met Gln Trp Asp Glu Ser Lys Asn Ala Gly Phe Ser  
 405 410 415  
 Thr Gly Gln Pro Trp Leu Ala Val Asn Pro Asn Tyr Glu Met Ile Asn  
 420 425 430  
 Val Gln Glu Ala Leu Ala Asn Pro Asp Ser Ile Phe Tyr Thr Tyr Gln  
 435 440 445  
 Lys Leu Val Gln Ile Arg Lys Glu Asn Ser Trp Leu Ile Arg Ala Asp  
 450 455 460  
 Phe Glu Leu Leu Asp Thr Ala Asp Lys Val Phe Ala Tyr Ile Arg Lys  
 465 470 475 480  
 Asp Gly Asp Arg Arg Phe Leu Val Val Ala Asn Leu Ser Asn Glu Glu  
 485 490 495  
 Gln Asp Leu Thr Val Glu Gly Lys Val Lys Ser Val Leu Ile Glu Asn  
 500 505 510  
 Thr Leu Ala Gln Glu Val Phe Glu Lys Gln Ile Leu Val Pro Trp Asp  
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 Ala Phe Cys Val Glu Leu Leu  
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<212> DNA

<213> Streptococcus pneumoniae

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21

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<212> DNA

<213> Streptococcus pneumoniae

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20